

10/521940

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SEQUENCE LISTING

<110> Yamanouchi Pharmaceutical Co., Ltd.  
Harigai, Masayoshi

<120> RA relating novel gene

<130> YHA0332-PCT

<150> JP2002-211951

<151> 2002-07-22

<160> 34

<170> PatentIn version 3.1

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(1071)

<223> Inventor: Takeuchi, Masahiro; Yamaji, Noboru; Takasaki, Jun;  
Akamatsu, Masahiko; Tsunoyama, Kazuhisa; Harigai, Masayoshi

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Asp Val Asp Ile Leu Gln Pro Ser Phe Asn Phe Leu Tyr Trp Ser Leu	
35 40 45	
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Ser Ser Thr Gly Leu Met Glu Leu Leu Glu Lys Met Leu Ala Leu Thr	
65 70 75 80	
ttg gca aag gca gat tct ccc agg act gca ctc ctc tgc tct gcc tgg	288
Leu Ala Lys Ala Asp Ser Pro Arg Thr Ala Leu Leu Cys Ser Ala Trp	
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ctg ctc act gcc tcc ttc tct gcc cag cag cac aag ggc agt ttg cag	336
Leu Leu Thr Ala Ser Phe Ser Ala Gln Gln His Lys Gly Ser Leu Gln	
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Val His Gln Thr Leu Ser Val Glu Met Asp Gln Val Leu Lys Ala Leu	
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Gln Asn Leu Leu Val Gln Lys Asp Pro Leu Leu Ser Gln Ala Cys Val	
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acc ctc ttg gat gct gga gag aat tcc ttc ctc aga cct gag att ttg	768
Thr Leu Leu Asp Ala Gly Glu Asn Ser Phe Leu Arg Pro Glu Ile Leu	
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275 280 285	
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Ser Thr Leu Ser Asn Thr Thr Leu Gln Ala Leu His Gly Phe Phe Gln	
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Gln Leu Gln Ser Met Gly His Leu Ala Asp His Ser Met Ala Gln Thr	
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Leu Leu Thr Ala Ser Phe Ser Ala Gln Gln His Lys Gly Ser Leu Gln  
 100 105 110

Val His Gln Thr Leu Ser Val Glu Met Asp Gln Val Leu Lys Ala Leu  
 115 120 125

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 130 135 140

Phe Leu Arg Thr Ala Leu Arg Gln Ser Phe Ser Ser Ala Leu Val Ala  
 145 150 155 160

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 165 170 175

Leu Ala Pro Leu Arg Met Ser Gln Val Arg Ser Leu Val Ile Gly Leu  
 180 185 190

Gln Asn Leu Leu Val Gln Lys Asp Pro Leu Leu Ser Gln Ala Cys Val  
 195 200 205

Gly Cys Leu Glu Ala Leu Leu Asp Tyr Leu Asp Ala Arg Ser Pro Asp  
 210 215 220

Ile Ala Leu His Val Ala Ser Gln Pro Trp Asn Arg Phe Leu Leu Phe  
 225 230 235 240

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 245 250 255

Arg Leu Met Thr Leu Phe Met Arg Tyr Arg Ser Ser Ser Val Leu Ser  
 260 265 270

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 275 280 285

Ser Thr Leu Ser Asn Thr Thr Leu Gln Ala Leu His Gly Phe Phe Gln  
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Gln Leu Gln Ser Met Gly His Leu Ala Asp His Ser Met Ala Gln Thr  
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Leu Gln Ala Ser Leu Glu Gly Leu Pro Pro Ser Thr Ser Ser Gly Gln  
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ccc aag gca gga gga agg gcg gcg ccc cca aac tcc cag gac gcc tgc 96  
Pro Lys Ala Gly Gly Arg Ala Ala Pro Pro Asn Ser Gln Asp Ala Cys  
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agc acc ccc cac gcg ccg ctc tcc gcc tct ggg gag cat cct gcc acc 144  
Ser Thr Pro His Ala Pro Leu Ser Ala Ser Gly Glu His Pro Ala Thr  
35 40 45  
  
ccc cga cac aca cac ccc ggc tac atc ccg cct tct cac gct tgg tca 192  
Pro Arg His Thr His Pro Gly Tyr Ile Pro Pro Ser His Ala Trp Ser  
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Gly Ala Leu Glu Met Ser Glu Ile Gln Ala Phe Pro Lys Glu Ser Gly  
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ttg gaa ggc gga ctc cca cgc ttt gct gag ctc cac atg aca aca gca 288  
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35 40 45

Pro Arg His Thr His Pro Gly Tyr Ile Pro Pro Ser His Ala Trp Ser  
50 55 60

Gly Ala Leu Glu Met Ser Glu Ile Gln Ala Phe Pro Lys Glu Ser Gly  
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 cgc ggg caa ctg gga gag ggg gcg gtg ccc agt tcc cgg ccc ggc cct 96  
 Arg Gly Gln Leu Gly Glu Gly Ala Val Pro Ser Ser Arg Pro Gly Pro  
                             20                            25                            30  
  
 ccc cgc gga ggt ggc cac gtc agc gca gcg tcg ctc gga gct cgc ggc 144  
 Pro Arg Gly Gly Gly His Val Ser Ala Ala Ser Leu Gly Ala Arg Gly  
                             35                            40                            45  
  
 cgg atg ggg aag gcg gcg gcg gcg gtg gcc ttt ggg gcc gaa gtg ggc 192  
 Arg Met Gly Lys Ala Ala Ala Val Ala Phe Gly Ala Glu Val Gly  
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 gtg cgg ctc gcg ctg ttc gcg gcc ttc ctg gtg acg gag ctg ctc ccc 240

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Val Arg Leu Ala Leu Phe Ala Ala Phe Leu Val Thr Glu Leu Leu Pro  
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Pro Phe Gln Arg Leu Ile Gln Pro Glu Glu Met Trp Leu Tyr Arg Asn  
85 90 95

ccc tac gtg gag gcg gag tat ttc ccc acc aag ccg atg ttt gtt att 336  
Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Lys Pro Met Phe Val Ile  
100 105 110

gca ttt ctc tct cca ctg tct ctg atc ttc ctg gcc aaa ttt ctc aag 384  
Ala Phe Leu Ser Pro Leu Ser Leu Ile Phe Leu Ala Lys Phe Leu Lys  
115 120 125

aag gca gac aca aga gac agc aga caa gcc tgc ctg gct gcc agc ctt 432  
Lys Ala Asp Thr Arg Asp Ser Arg Gln Ala Cys Leu Ala Ala Ser Leu  
130 135 140

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Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe Pro Asp Gly Leu  
165 170 175

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Ala His Ser Asp Leu Met Cys Thr Gly Asp Lys Asp Val Val Asn Glu  
180 185 190

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Gly Arg Lys Ser Phe Pro Ser Gly His Ser Ser Phe Ala Phe Ala Gly  
195 200 205

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Leu Ala Phe Ala Ser Phe Tyr Leu Ala Gly Lys Leu His Cys Phe Thr  
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 225 230 235 240

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gcc tat gtc tgc tat cgg cag tat tat cct cct ctg act gat gca gaa 864  
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tgc cat aaa cca ttt caa gac aaa ctt gta ctt tcc act gca cag aag 912  
 Cys His Lys Pro Phe Gln Asp Lys Leu Val Leu Ser Thr Ala Gln Lys  
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Arg Met Gly Lys Ala Ala Ala Ala Val Ala Phe Gly Ala Glu Val Gly  
50 55 60

Val Arg Leu Ala Leu Phe Ala Ala Phe Leu Val Thr Glu Leu Leu Pro  
65 70 75 80

Pro Phe Gln Arg Leu Ile Gln Pro Glu Glu Met Trp Leu Tyr Arg Asn  
85 90 95

Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Lys Pro Met Phe Val Ile  
100 105 110

Ala Phe Leu Ser Pro Leu Ser Leu Ile Phe Leu Ala Lys Phe Leu Lys  
115 120 125

Lys Ala Asp Thr Arg Asp Ser Arg Gln Ala Cys Leu Ala Ala Ser Leu  
130 135 140

Ala Leu Ala Leu Asn Gly Val Phe Thr Asn Thr Ile Lys Leu Ile Val



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 Arg Leu Ala Leu Phe Ala Ala Phe Leu Val Thr Glu Leu Leu Pro Pro  
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 Phe Gln Arg Leu Ile Gln Pro Glu Glu Met Trp Leu Tyr Arg Asn Pro  
 35 40 45  
 tac gtg gag gcg gag tat ttc ccc acc aag ccg atg ttt gtt att gca 192  
 Tyr Val Glu Ala Glu Tyr Phe Pro Thr Lys Pro Met Phe Val Ile Ala  
 50 55 60  
 ttt ctc tct cca ctg tct ctg atc ttc ctg gcc aaa ttt ctc aag aag 240  
 Phe Leu Ser Pro Leu Ser Leu Ile Phe Leu Ala Lys Phe Leu Lys Lys

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	85	90	95	
ctg gct ctg aat ggc gtc ttt acc aac aca ata aaa ctg atc gta ggg				336
Leu Ala Leu Asn Gly Val Phe Thr Asn Thr Ile Lys Leu Ile Val Gly				
	100	105	110	
agg cca cgc cca gat ttc ttc tac cgc tgc ttc cct gat ggg cta gcc				384
Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe Pro Asp Gly Leu Ala				
	115	120	125	
cat tct gac ttg atg tgt aca ggg gat aag gac gtg gtg aat gag ggc				432
His Ser Asp Leu Met Cys Thr Gly Asp Lys Asp Val Val Asn Glu Gly				
	130	135	140	
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Arg Lys Ser Phe Pro Ser Gly His Ser Ser Phe Ala Phe Ala Gly Leu				
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gcc ttt ggc tcc ttc tac ctg gca ggg aag tta cac tgc ttc aca cca				528
Ala Phe Ala Ser Phe Tyr Leu Ala Gly Lys Leu His Cys Phe Thr Pro				
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caa ggc cgt ggg aaa tct tgg agg ttc tgt gcc ttt ctg tca cct cta				576
Gln Gly Arg Gly Lys Ser Trp Arg Phe Cys Ala Phe Leu Ser Pro Leu				
	180	185	190	
ctt ttt gca gct gtg att gca ctg tcc cgc aca tgt gac tac aag cat				624
Leu Phe Ala Ala Val Ile Ala Leu Ser Arg Thr Cys Asp Tyr Lys His				
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Phe Gln Arg Leu Ile Gln Pro Glu Glu Met Trp Leu Tyr Arg Asn Pro  
35 40 45

Tyr Val Glu Ala Glu Tyr Phe Pro Thr Lys Pro Met Phe Val Ile Ala  
50 55 60



Phe Leu Ser Pro Leu Ser Leu Ile Phe Leu Ala Lys Phe Leu Lys Lys  
 65 70 75 80

Ala Asp Thr Arg Asp Ser Arg Gln Ala Cys Leu Ala Ala Ser Leu Ala  
 85 90 95

Leu Ala Leu Asn Gly Val Phe Thr Asn Thr Ile Lys Leu Ile Val Gly  
 100 105 110

Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe Pro Asp Gly Leu Ala  
 115 120 125

His Ser Asp Leu Met Cys Thr Gly Asp Lys Asp Val Val Asn Glu Gly  
 130 135 140

Arg Lys Ser Phe Pro Ser Gly His Ser Ser Phe Ala Phe Ala Gly Leu  
 145 150 155 160

Ala Phe Ala Ser Phe Tyr Leu Ala Gly Lys Leu His Cys Phe Thr Pro  
 165 170 175

Gln Gly Arg Gly Lys Ser Trp Arg Phe Cys Ala Phe Leu Ser Pro Leu  
 180 185 190

Leu Phe Ala Ala Val Ile Ala Leu Ser Arg Thr Cys Asp Tyr Lys His  
 195 200 205

His Trp Gln Asp Val Leu Val Gly Ser Met Ile Gly Met Thr Phe Ala  
 210 215 220

Tyr Val Cys Tyr Arg Gln Tyr Tyr Pro Pro Leu Thr Asp Ala Glu Cys  
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 Ser Gly Arg Thr Met Arg Glu Leu Ala Ile Glu Ile Gly Val Arg Ala  
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35 40 45	
aga gtc atc cag cca gaa gag atc tgg ctc tat aaa aat cct ttg gtg	192
Arg Val Ile Gln Pro Glu Glu Ile Trp Leu Tyr Lys Asn Pro Leu Val	
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caa tca gat aac ata cct acc cgc ctc atg ttt gca att tct ttc ctc	240
Gln Ser Asp Asn Ile Pro Thr Arg Leu Met Phe Ala Ile Ser Phe Leu	
65 70 75 80	
aca ccc ctg gct gtt att tgt gtg gtg aaa att atc cgg cga aca gac	288
Thr Pro Leu Ala Val Ile Cys Val Val Lys Ile Ile Arg Arg Thr Asp	
85 90 95	
aag act gaa att aag gaa gcc ttc tta gcg gtg tcc ttg gct ott gct	336
Lys Thr Glu Ile Lys Glu Ala Phe Leu Ala Val Ser Leu Ala Leu Ala	
100 105 110	
ttg aat gga gtc tgc aca aac act att aaa tta ata gtg gga aga cct	384
Leu Asn Gly Val Cys Thr Asn Thr Ile Lys Leu Ile Val Gly Arg Pro	
115 120 125	
cgc ccc gat ttc ttt tac cgc tgc ttt cca gat gga gtg atg aac tcg	432
Arg Pro Asp Phe Phe Tyr Arg Cys Phe Pro Asp Gly Val Met Asn Ser	
130 135 140	
gaa atg cat tgc aca ggt gac ccc gat ctg gtg tcc gag ggc cgc aaa	480
Glu Met His Cys Thr Gly Asp Pro Asp Leu Val Ser Glu Gly Arg Lys	
145 150 155 160	
agc ttc ccc agc atc cat tcc tcc ttt gcc ttt tcg ggc ctt ggc ttc	528
Ser Phe Pro Ser Ile His Ser Ser Phe Ala Phe Ser Gly Leu Gly Phe	
165 170 175	

acg acg ttc tac ttg gcg ggc aag ctg cac tgc ttc acc gag agt ggg 576  
 Thr Thr Phe Tyr Leu Ala Gly Lys Leu His Cys Phe Thr Glu Ser Gly  
 180 185 190

cgg gga aag agc tgg cgg ctc tgt gct gcc atc ctg ccc ttg tac tgc 624  
 Arg Gly Lys Ser Trp Arg Leu Cys Ala Ala Ile Leu Pro Leu Tyr Cys  
 195 200 205

gcc atg atg att gcc ctg tcc cgc atg tgc gac tac aag cat cac tgg 672  
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 210 215 220

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tgc tac aga cag cac tat cct cct ctg gcc aac aca gct tgc cat aaa 768  
 Cys Tyr Arg Gln His Tyr Pro Pro Leu Ala Asn Thr Ala Cys His Lys  
 245 250 255

ccc tac gtt agt ctg cga gtc cca gcc tca ctg aag aaa gag gag agg 816  
 Pro Tyr Val Ser Leu Arg Val Pro Ala Ser Leu Lys Lys Glu Glu Arg  
 260 265 270

ccc aca gct gac agc gca ccc agc ttg cct ctg gag ggg atc acc gaa 864  
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 275 280 285

ggc ccg gta tga 876  
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&lt;213&gt; Homo sapiens

&lt;400&gt; 10

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Ser	Gly	Arg	Thr	Met	Arg	Glu	Leu	Ala	Ile	Glu	Ile	Gly	Val	Arg	Ala
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Leu	Leu	Phe	Gly	Val	Phe	Val	Phe	Thr	Glu	Phe	Leu	Asp	Pro	Phe	Gln
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Lys	Thr	Glu	Ile	Lys	Glu	Ala	Phe	Leu	Ala	Val	Ser	Leu	Ala	Leu	Ala
				100				105					110		

Leu	Asn	Gly	Val	Cys	Thr	Asn	Thr	Ile	Lys	Leu	Ile	Val	Gly	Arg	Pro
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 130 135 140

Glu Met His Cys Thr Gly Asp Pro Asp Leu Val Ser Glu Gly Arg Lys  
 145 150 155 160

Ser Phe Pro Ser Ile His Ser Ser Phe Ala Phe Ser Gly Leu Gly Phe  
 165 170 175

Thr Thr Phe Tyr Leu Ala Gly Lys Leu His Cys Phe Thr Glu Ser Gly  
 180 185 190

Arg Gly Lys Ser Trp Arg Leu Cys Ala Ala Ile Leu Pro Leu Tyr Cys  
 195 200 205

Ala Met Met Ile Ala Leu Ser Arg Met Cys Asp Tyr Lys His His Trp  
 210 215 220

Gln Asp Ser Phe Val Gly Gly Val Ile Gly Leu Ile Phe Ala Tyr Ile  
 225 230 235 240

Cys Tyr Arg Gln His Tyr Pro Pro Leu Ala Asn Thr Ala Cys His Lys  
 245 250 255

Pro Tyr Val Ser Leu Arg Val Pro Ala Ser Leu Lys Lys Glu Glu Arg  
 260 265 270

Pro Thr Ala Asp Ser Ala Pro Ser Leu Pro Leu Glu Gly Ile Thr Glu  
 275 280 285

Gly Pro Val  
 290

<210> 11  
 <211> 816  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(813)  
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<400> 11  
 atg cgg gag ctg gcc att gag atc ggg gtg cga gcc ctg ctc ttc gga 48  
 Met Arg Glu Leu Ala Ile Glu Ile Gly Val Arg Ala Leu Leu Phe Gly  
 1 5 10 15

gtc ttc gtt ttt aca gag ttt ttg gat ccg ttc cag aga gtc atc cag 96  
 Val Phe Val Phe Thr Glu Phe Leu Asp Pro Phe Gln Arg Val Ile Gln  
 20 25 30

cca gaa gag atc tgg ctc tat aaa aat cct ttg gtg caa tca gat aac 144  
 Pro Glu Glu Ile Trp Leu Tyr Lys Asn Pro Leu Val Gln Ser Asp Asn  
 35 40 45

ata cct acc cgc ctc atg ttt gca att tct ttc ctc aca ccc ctg gct 192  
 Ile Pro Thr Arg Leu Met Phe Ala Ile Ser Phe Leu Thr Pro Leu Ala  
 50 55 60

gtt att tgt gtg gtg aaa att atc cgg cga aca gac aag act gaa att 240  
Val Ile Cys Val Val Lys Ile Ile Arg Arg Thr Asp Lys Thr Glu Ile  
65 70 75 80

aag gaa gcc ttc tta gcg gtg tcc ttg gct ctt gct ttg aat gga gtc 288  
Lys Glu Ala Phe Leu Ala Val Ser Leu Ala Leu Ala Leu Asn Gly Val  
85 90 95

tgc aca aac act att aaa tta ata gtg gga aga cct cgc ccc gat ttc 336  
Cys Thr Asn Thr Ile Lys Leu Ile Val Gly Arg Pro Arg Pro Asp Phe  
100 105 110

ttt tac cgc tgc ttt cca gat gga gtg atg aac tcg gaa atg cat tgc 384  
Phe Tyr Arg Cys Phe Pro Asp Gly Val Met Asn Ser Glu Met His Cys  
115 120 125

aca ggt gac ccc gat ctg gtg tcc gag ggc cgc aaa agc ttc ccc agc 432  
Thr Gly Asp Pro Asp Leu Val Ser Glu Gly Arg Lys Ser Phe Pro Ser  
130 135 140

atc cat tcc tcc ttt gcc ttt tcg ggc ctt ggc ttc acg acg ttc tac 480  
Ile His Ser Ser Phe Ala Phe Ser Gly Leu Gly Phe Thr Thr Phe Tyr  
145 150 155 160

ttg gcg ggc aag ctg cac tgc ttc acc gag agt ggg cgg gga aag agc 528  
Leu Ala Gly Lys Leu His Cys Phe Thr Glu Ser Gly Arg Gly Lys Ser  
165 170 175

tgg cgg ctc tgt gct gcc atc ctg ccc ttg tac tgc gcc atg atg att 576  
Trp Arg Leu Cys Ala Ala Ile Leu Pro Leu Tyr Cys Ala Met Met Ile  
180 185 190

gcc ctg tcc cgc atg tgc gac tac aag cat cac tgg caa gat tcc ttt 624  
Ala Leu Ser Arg Met Cys Asp Tyr Lys His His Trp Gln Asp Ser Phe  
195 200 205



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gtg ggt gga gtc atc ggc ctc att ttt gca tac att tgc tac aga cag 672  
Val Gly Gly Val Ile Gly Leu Ile Phe Ala Tyr Ile Cys Tyr Arg Gln  
210 215 220

cac tat cct cct ctg gcc aac aca gct tgc cat aaa ccc tac gtt agt 720  
His Tyr Pro Pro Leu Ala Asn Thr Ala Cys His Lys Pro Tyr Val Ser  
225 230 235 240

ctg cga gtc cca gcc tca ctg aag aaa gag gag agg ccc aca gct gac 768  
Leu Arg Val Pro Ala Ser Leu Lys Lys Glu Glu Arg Pro Thr Ala Asp  
245 250 255

agc gca ccc agc ttg cct ctg gag ggg atc acc gaa ggc ccg gta tga 816  
Ser Ala Pro Ser Leu Pro Leu Glu Gly Ile Thr Glu Gly Pro Val  
260 265 270

<210> 12

<211> 271

<212> PRT

<213> Homo sapiens

<400> 12

Met Arg Glu Leu Ala Ile Glu Ile Gly Val Arg Ala Leu Leu Phe Gly  
1 5 10 15

Val Phe Val Phe Thr Glu Phe Leu Asp Pro Phe Gln Arg Val Ile Gln  
20 25 30

Pro Glu Glu Ile Trp Leu Tyr Lys Asn Pro Leu Val Gln Ser Asp Asn  
35 40 45

Ile Pro Thr Arg Leu Met Phe Ala Ile Ser Phe Leu Thr Pro Leu Ala  
 50 55 60

Val Ile Cys Val Val Lys Ile Ile Arg Arg Thr Asp Lys Thr Glu Ile  
 65 70 75 80

Lys Glu Ala Phe Leu Ala Val Ser Leu Ala Leu Ala Leu Asn Gly Val  
 85 90 95

Cys Thr Asn Thr Ile Lys Leu Ile Val Gly Arg Pro Arg Pro Asp Phe  
 100 105 110

Phe Tyr Arg Cys Phe Pro Asp Gly Val Met Asn Ser Glu Met His Cys  
 115 120 125

Thr Gly Asp Pro Asp Leu Val Ser Glu Gly Arg Lys Ser Phe Pro Ser  
 130 135 140

Ile His Ser Ser Phe Ala Phe Ser Gly Leu Gly Phe Thr Thr Phe Tyr  
 145 150 155 160

Leu Ala Gly Lys Leu His Cys Phe Thr Glu Ser Gly Arg Gly Lys Ser  
 165 170 175

Trp Arg Leu Cys Ala Ala Ile Leu Pro Leu Tyr Cys Ala Met Met Ile  
 180 185 190

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Ala Leu Ser Arg Met Cys Asp Tyr Lys His His Trp Gln Asp Ser Phe  
195 200 205

Val Gly Gly Val Ile Gly Leu Ile Phe Ala Tyr Ile Cys Tyr Arg Gln  
210 215 220

His Tyr Pro Pro Leu Ala Asn Thr Ala Cys His Lys Pro Tyr Val Ser  
225 230 235 240

Leu Arg Val Pro Ala Ser Leu Lys Lys Glu Glu Arg Pro Thr Ala Asp  
245 250 255

Ser Ala Pro Ser Leu Pro Leu Glu Gly Ile Thr Glu Gly Pro Val  
260 265 270

<210> 13

<211> 37

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

<400> 13

cgcgcggtac cgccaccatg cagctcagga atgtgtc

37

<210> 14

<211> 31

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 14

gcgcgctcga ggtttctgat gtgggacagg g

31

<210> 15

<211> 37

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 15

gcgcgaagct tgccaccatg cctagaaggg gaccaca

37

<210> 16

<211> 30

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 16

gcgcgctcga ggtgcggcct gtcgtctgct

30

<210> 17  
<211> 35  
<212> DNA  
<213> Artificial

<220>

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

<400> 17  
gcgcgaagct tgccaccatg ccctoggcac agccg

35

<210> 18  
<211> 35  
<212> DNA  
<213> Artificial

<220>

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

<400> 18  
gcgcgctcga gaatatcaaa acaataagaa tcccc

35

<210> 19  
<211> 35  
<212> DNA  
<213> Artificial

<220>

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

<400> 19

gcgcgaagct tgccaccatg gggaaggcgg cggcg

35

<210> 20

<211> 35

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

<400> 20

gcgcgaagct tgccaccatg gctgcgggag cgcgc

35

<210> 21

<211> 30

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

<400> 21

gcgcgctcga gtaccgggcc ttcggtgatc

30

<210> 22

<211> 36

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence:an artificially

## synthesized primer sequence

&lt;400&gt; 22

gcgcgaagct tgccaccatg cgggagctgg ccattg

36

&lt;210&gt; 23

&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

&lt;400&gt; 23

tcgaggacta caaggacgac gatgacaagc t

31

&lt;210&gt; 24

&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

<223> Description of Artificial Sequence:an artificially  
synthesized primer sequence

&lt;400&gt; 24

ctagagcttg tcacgctcgt ccttgtagtc c

31

&lt;210&gt; 25

&lt;211&gt; 16

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 25  
cacgtggcct cccagc 16

<210> 26  
<211> 24  
<212> DNA  
<213> Homo sapiens

<400> 26  
taggttctcc catttgctgt tttt 24

<210> 27  
<211> 20  
<212> DNA  
<213> Homo sapiens

<400> 27  
cccttgaaca acgcaggttc 20

<210> 28  
<211> 20  
<212> DNA  
<213> Homo sapiens

<400> 28  
tttgtaggga caccacctg 20

<210> 29  
<211> 21  
<212> DNA  
<213> Homo sapiens



<400> 29  
cttccaaggt gcaagtgagg a 21

<210> 30  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 30  
cattggaggc agaatacagt gtg 23

<210> 31  
<211> 20  
<212> DNA  
<213> Homo sapiens

<400> 31  
tcctgggagg atggacacta 20

<210> 32  
<211> 21  
<212> DNA  
<213> Homo sapiens

<400> 32  
tgatgtcagg gtggcagatg t 21

<210> 33  
<211> 18  
<212> DNA  
<213> Homo sapiens

<400> 33

gggaagggtga aggtcgga

18

<210> 34

<211> 17

<212> DNA

<213> Homo sapiens

<400> 34

gcagccctgg tgaccag

17